

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/577,008  
Source: 1FWD  
Date Processed by STIC: 1/19/07

# **ENTERED**



IFWO

**RAW SEQUENCE LISTING** DATE: 01/19/2007  
**PATENT APPLICATION:** US/10/577,008 TIME: 16:40:54

Input Set : A:\2007-01-11 3749-0112PUS1.txt  
Output Set: N:\CRF4\01192007\J577008.raw

3 <110> APPLICANT: SUZUKI, Toshiharu et al.  
5 <120> TITLE OF INVENTION: MARKER PEPTIDE FOR ALZHEIMER'S DISEASE  
7 <130> FILE REFERENCE: 3749-0112PUS1  
9 <140> CURRENT APPLICATION NUMBER: US 10/577,008  
10 <141> CURRENT FILING DATE: 2006-04-25  
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/016209  
13 <151> PRIOR FILING DATE: 2004-11-01  
15 <150> PRIOR APPLICATION NUMBER: JP 2003/375363  
16 <151> PRIOR FILING DATE: 2003-11-05  
18 <160> NUMBER OF SEQ ID NOS: 13  
20 <170> SOFTWARE: PatentIn Ver. 2.0  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 971  
24 <212> TYPE: PRT  
25 <213> ORGANISM: human  
27 <400> SEQUENCE: 1  
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31 Leu Ala Gly Leu Leu Cys Gly Gly Val Trp Ala Ala Arg Val Asn  
32   20              25                   30  
34 Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly Ile Val Thr Glu  
35   35              40                  45  
37 Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu Ile Ala Leu Asp Lys  
38   50              55                  60  
40 Asp Ala Pro Leu Arg Phe Ala Gly Glu Ile Cys Gly Phe Lys Ile His  
41   65              70                  75                  80  
43 Gly Gln Asn Val Pro Phe Asp Ala Val Val Val Asp Lys Ser Thr Gly  
44   85              90                  95  
46 Glu Gly Val Ile Arg Ser Lys Glu Lys Leu Asp Cys Glu Leu Gln Lys  
47   100             105                110  
49 Asp Tyr Ser Phe Thr Ile Gln Ala Tyr Asp Cys Gly Lys Gly Pro Asp  
50   115             120                125  
52 Gly Thr Asn Val Lys Lys Ser His Lys Ala Thr Val His Ile Gln Val  
53   130             135                140  
55 Asn Asp Val Asn Glu Tyr Ala Pro Val Phe Lys Glu Lys Ser Tyr Lys  
56 145             150                155                  160  
58 Ala Thr Val Ile Glu Gly Lys Gln Tyr Asp Ser Ile Leu Arg Val Glu  
59   165             170                175  
61 Ala Val Asp Ala Asp Cys Ser Pro Gln Phe Ser Gln Ile Cys Ser Tyr  
62   180             185                190  
64 Glu Ile Ile Thr Pro Asp Val Pro Phe Thr Val Asp Lys Asp Gly Tyr  
65   195             200                205  
67 Ile Lys Asn Thr Glu Lys Leu Asn Tyr Gly Lys Glu His Gln Tyr Lys

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68	210	215	220
70	Leu Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala Thr Glu Asp		
71	225	230	235
			240
73	Val Leu Val Lys Ile Ser Ile Lys Pro Thr Cys Thr Pro Gly Trp Gln		
74	245	250	255
76	Gly Trp Asn Asn Arg Ile Glu Tyr Glu Pro Gly Thr Gly Ala Leu Ala		
77	260	265	270
79	Val Phe Pro Asn Ile His Leu Glu Thr Cys Asp Glu Pro Val Ala Ser		
80	275	280	285
82	Val Gln Ala Thr Val Glu Leu Glu Thr Ser His Ile Gly Lys Gly Cys		
83	290	295	300
85	Asp Arg Asp Thr Tyr Ser Glu Lys Ser Leu His Arg Leu Cys Gly Ala		
86	305	310	315
			320
88	Ala Ala Gly Thr Ala Glu Leu Leu Pro Ser Pro Ser Gly Ser Leu Asn		
89	325	330	335
91	Trp Thr Met Gly Leu Pro Thr Asp Asn Gly His Asp Ser Asp Gln Val		
92	340	345	350
94	Phe Glu Phe Asn Gly Thr Gln Ala Val Arg Ile Pro Asp Gly Val Val		
95	355	360	365
97	Ser Val Ser Pro Lys Glu Pro Phe Thr Ile Ser Val Trp Met Arg His		
98	370	375	380
100	Gly Pro Phe Gly Arg Lys Lys Glu Thr Ile Leu Cys Ser Ser Asp Lys		
101	385	390	395
			400
103	Thr Asp Met Asn Arg His His Tyr Ser Leu Tyr Val His Gly Cys Arg		
104	405	410	415
106	Leu Ile Phe Leu Phe Arg Gln Asp Pro Ser Glu Glu Lys Lys Tyr Arg		
107	420	425	430
109	Pro Ala Glu Phe His Trp Lys Leu Asn Gln Val Cys Asp Glu Glu Trp		
110	435	440	445
112	His His Tyr Val Leu Asn Val Glu Phe Pro Ser Val Thr Leu Tyr Val		
113	450	455	460
115	Asp Gly Thr Ser His Glu Pro Phe Ser Val Thr Glu Asp Tyr Pro Leu		
116	465	470	475
			480
118	His Pro Ser Lys Ile Glu Thr Gln Leu Val Val Gly Ala Cys Trp Gln		
119	485	490	495
121	Glu Phe Ser Gly Val Glu Asn Asp Asn Glu Thr Glu Pro Val Thr Val		
122	500	505	510
124	Ala Ser Ala Gly Gly Asp Leu His Met Thr Gln Phe Phe Arg Gly Asn		
125	515	520	525
127	Leu Ala Gly Leu Thr Leu Arg Ser Gly Lys Leu Ala Asp Lys Lys Val		
128	530	535	540
130	Ile Asp Cys Leu Tyr Thr Cys Lys Glu Gly Leu Asp Leu Gln Val Leu		
131	545	550	555
			560
133	Glu Asp Ser Gly Arg Gly Val Gln Ile Gln Ala His Pro Ser Gln Leu		
134	565	570	575
136	Val Leu Thr Leu Glu Gly Glu Asp Leu Gly Glu Leu Asp Lys Ala Met		
137	580	585	590
139	Gln His Ile Ser Tyr Leu Asn Ser Arg Gln Phe Pro Thr Pro Gly Ile		
140	595	600	605

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142 Arg Arg Leu Lys Ile Thr Ser Thr Ile Lys Cys Phe Asn Glu Ala Thr  
 143 610 615 620  
 145 Cys Ile Ser Val Pro Pro Val Asp Gly Tyr Val Met Val Leu Gln Pro  
 146 625 630 635 640  
 148 Glu Glu Pro Lys Ile Ser Leu Ser Gly Val His His Phe Ala Arg Ala  
 149 645 650 655  
 151 Ala Ser Glu Phe Glu Ser Ser Glu Gly Val Phe Leu Phe Pro Glu Leu  
 152 660 665 670  
 154 Arg Ile Ile Ser Thr Ile Thr Arg Glu Val Glu Pro Glu Gly Asp Gly  
 155 675 680 685  
 157 Ala Glu Asp Pro Thr Val Gln Glu Ser Leu Val Ser Glu Glu Ile Val  
 158 690 695 700  
 160 His Asp Leu Asp Thr Cys Glu Val Thr Val Glu Gly Glu Glu Leu Asn  
 161 705 710 715 720  
 163 His Glu Gln Glu Ser Leu Glu Val Asp Met Ala Arg Leu Gln Gln Lys  
 164 725 730 735  
 166 Gly Ile Glu Val Ser Ser Ser Glu Leu Gly Met Thr Phe Thr Gly Val  
 167 740 745 750  
 169 Asp Thr Met Ala Ser Tyr Glu Glu Val Leu His Leu Leu Arg Tyr Arg  
 170 755 760 765  
 172 Asn Trp His Ala Arg Ser Leu Leu Asp Arg Lys Phe Lys Leu Ile Cys  
 173 770 775 780  
 175 Ser Glu Leu Asn Gly Arg Tyr Ile Ser Asn Glu Phe Lys Val Glu Val  
 176 785 790 795 800  
 178 Asn Val Ile His Thr Ala Asn Pro Met Glu His Ala Asn His Met Ala  
 179 805 810 815  
 181 Ala Gln Pro Gln Phe Val His Pro Glu His Arg Ser Phe Val Asp Leu  
 182 820 825 830  
 184 Ser Gly His Asn Leu Ala Asn Pro His Pro Phe Ala Val Val Pro Ser  
 185 835 840 845  
 187 Thr Ala Thr Val Val Ile Val Val Cys Val Ser Phe Leu Val Phe Met  
 188 850 855 860  
 190 Ile Ile Leu Gly Val Phe Arg Ile Arg Ala Ala His Arg Arg Thr Met  
 191 865 870 875 880  
 193 Arg Asp Gln Asp Thr Gly Lys Glu Asn Glu Met Asp Trp Asp Asp Ser  
 194 885 890 895  
 196 Ala Leu Thr Ile Thr Val Asn Pro Met Glu Thr Tyr Glu Asp Gln His  
 197 900 905 910  
 199 Ser Ser Glu Glu Glu Glu Glu Glu Glu Glu Ser Glu Asp  
 200 915 920 925  
 202 Gly Glu Glu Glu Asp Asp Ile Thr Ser Ala Glu Ser Glu Ser Ser Glu  
 203 930 935 940  
 205 Glu Glu Glu Gly Glu Gln Gly Asp Pro Gln Asn Ala Thr Arg Gln Gln  
 206 945 950 955 960  
 208 Gln Leu Glu Trp Asp Asp Ser Thr Leu Ser Tyr  
 209 965 970  
 211 <210> SEQ ID NO: 2  
 212 <211> LENGTH: 968  
 213 <212> TYPE: PRT

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214 <213> ORGANISM: human  
 216 <400> SEQUENCE: 2  
 217 Met Val Leu Gly Cys Glu Leu Ser Gly Ser Thr Arg Val Val Val Gly  
     1               5                 10                 15  
 220 Val Glu Ala Leu Leu Thr Gly Ala Ser Ser Pro Leu Pro Gly Val Gly  
     20               25                 30  
 223 Pro Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu Tyr Gln Gly Ile  
     35               40                 45  
 226 Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro Pro Leu Phe Ala  
     50               55                 60  
 229 Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu Ile Cys Gly Phe  
     65               70                 75                 80  
 232 Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val Ile Leu Asp Lys  
     85               90                 95  
 235 Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro Val Asp Cys Glu  
     100              105                 110  
 238 Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr Asp Cys Gly Glu  
     115              120                 125  
 241 Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys Ala Thr Val His  
     130              135                 140  
 244 Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val Phe Val Glu Arg  
     145              150                 155                 160  
 247 Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr Asp Arg Ile Leu  
     165              170                 175  
 250 Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln Tyr Ser Gln Ile  
     180              185                 190  
 253 Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe Leu Ile Asp Asn  
     195              200                 205  
 256 Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr Ser Gly Glu Arg  
     210              215                 220  
 259 Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala  
     225              230                 235                 240  
 262 Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro Thr Cys Lys Pro  
     245              250                 255  
 265 Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala Pro Gly Ala Gly  
     260              265                 270  
 268 Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr Cys Asp Glu Pro  
     275              280                 285  
 271 Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr Ser His Val Ala  
     290              295                 300  
 274 Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala Leu Arg Lys Leu  
     305              310                 315                 320  
 277 Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro Met Pro Gly Pro  
     325              330                 335  
 280 Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr Ser Gln Asp Ser  
     340              345                 350  
 283 Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val Gln Val Pro Leu  
     355              360                 365  
 286 Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp Ser Leu Ser Asp

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287	370	375	380
289	His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val Thr Pro Asn Lys		
290	385	390	395
292	Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr Val Gln Asn Glu		400
293	405	410	415
295	Asp Gly Phe Ser His Tyr Ser Leu Thr Val His Gly Cys Arg Ile Ala		
296	420	425	430
298	Phe Leu Tyr Trp Pro Leu Leu Glu Ser Ala Arg Pro Val Lys Phe Leu		
299	435	440	445
301	Trp Lys Leu Glu Gln Val Cys Asp Asp Glu Trp His His Tyr Ala Leu		
302	450	455	460
304	Asn Leu Glu Phe Pro Thr Val Thr Leu Tyr Thr Asp Gly Ile Ser Phe		
305	465	470	475
307	480	485	490
308	Asp Pro Ala Leu Ile His Asp Asn Gly Leu Ile His Pro Pro Arg Arg		495
310	Glu Pro Ala Leu Met Ile Gly Ala Cys Trp Thr Glu Glu Lys Asn Lys		
311	500	505	510
313	Glu Lys Glu Lys Gly Asp Asn Ser Thr Asp Thr Thr Gln Gly Asp Pro		
314	515	520	525
316	Leu Ser Ile His His Tyr Phe His Gly Tyr Leu Ala Gly Phe Ser Val		
317	530	535	540
319	Arg Ser Gly Arg Leu Glu Ser Arg Glu Val Ile Glu Cys Leu Tyr Ala		
320	545	550	555
322	Cys Arg Glu Gly Leu Asp Tyr Arg Asp Phe Glu Ser Leu Gly Lys Gly		560
323	565	570	575
325	Met Lys Val His Val Asn Pro Ser Gln Ser Leu Leu Thr Leu Glu Gly		
326	580	585	590
328	Asp Asp Val Glu Thr Phe Asn His Ala Leu Gln His Val Ala Tyr Met		
329	595	600	605
331	Asn Thr Leu Arg Phe Ala Thr Pro Gly Val Arg Pro Leu Arg Leu Thr		
332	610	615	620
334	Thr Ala Val Lys Cys Phe Ser Glu Glu Ser Cys Val Ser Ile Pro Glu		
335	625	630	635
337	640	645	650
338	Val Glu Gly Tyr Val Val Val Leu Gln Pro Asp Ala Pro Gln Ile Leu		655
340	660	665	670
341	Leu Ser Gly Thr Ala His Phe Ala Arg Pro Ala Val Asp Phe Glu Gly		
343	675	680	685
344	Thr Asn Gly Val Pro Leu Phe Pro Asp Leu Gln Ile Thr Cys Ser Ile		
346	Ser His Gln Val Glu Ala Lys Lys Asp Glu Ser Trp Gln Gly Thr Val		
347	690	695	700
349	705	710	715
352	720	725	730
355	Glu Ile Ser Leu Val Gly Asp Asp Leu Asp Pro Glu Arg Glu Ser Leu		735
356	740	745	750
358	Leu Leu Asp Thr Thr Ser Leu Gln Gln Arg Gly Leu Glu Leu Thr Asn		
359	755	760	765

**VERIFICATION SUMMARY**

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